

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 5.66667 Seconds
(without alignments)
91.287 Million cell updates/sec

Title: US-09-743-225-4

Perfect score: 62

Sequence: 1 KDKATFGTHDG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	90.3	345	1 APOH_HUMAN	P02749 homo sapien
2	46	74.2	345	1 APOH_MOUSE	Q01339 mus musculus
3	42	67.7	1310	1 YB35_SCHPO	O14340 schizosacch
4	41	66.1	297	1 APOH_RAT	P26644 rattus norv
5	41	66.1	345	1 APOH_CANFA	P33703 canis famil
6	40	64.5	345	1 APOH_BOVIN	P17690 bos taurus
7	40	64.5	363	1 DP3B_SPICI	P34029 spiroplasma
8	38	61.3	283	1 F123_CORVE	O74631 coriolus ve
9	37	59.7	537	1 DEXB_STREQ	Q59905 streptococ
10	36	58.1	307	1 Y690_VIBCH	Q9KU39 vibrio chol
11	36	58.1	417	1 TRMU_YEAST	Q12093 saccharomyc
12	36	58.1	477	1 FTBB_PETWA	P02678 petromyzon
13	36	58.1	496	1 CWLB_BACSU	Q02114 bacillus su
14	36	58.1	798	1 PHSG_BACSU	P39123 bacillus su
15	36	58.1	964	1 UH70_MCMVS	Q69153 murine cyto
16	35	56.5	198	1 IFE2_ARATH	O04663 arabidopsis
17	35	56.5	241	1 PYRH_HALNI	Q9HNN8 halobacteri
18	35	56.5	574	1 SYR_BUCAI	O44683 buchnera ap
19	35	56.5	962	1 UL52_PVRKA	Q85228 pseudorabie
20	35	56.5	2209	1 KNVC_HUMAN	P50748 homo sapien
21	34	54.8	151	1 GLB8_CHITH	P02227 chironomus
22	34	54.8	162	1 GLB6_CHITH	P02224 chironomus
23	34	54.8	366	1 QJEA_CAUCC	Q9A7V2 caulobacter
24	34	54.8	373	1 YSAK_CAEEL	Q93454 caenorhabdi
25	34	54.8	398	1 CGL_MOUSE	Q8VGN5 mus musculus
26	34	54.8	415	1 RF11_METAC	Q8TUM4 methanosarc
27	34	54.8	418	1 YMI3_YEAST	Q04526 saccharomyc
28	34	54.8	644	1 XYND_CELFI	P54865 cellulomona
29	34	54.8	699	1 MALQ_HAEIN	P45176 haemophilus
30	34	54.8	937	1 SYL_ECOLI	P00956 escherichia
31	34	54.8	973	1 UVRA_RHIME	P56899 rhizobium m
32	33	53.2	145	1 GLB7_CHITH	P02226 chironomus
33	33	53.2	161	1 GLB9_CHITH	P02223 chironomus

34	33	53.2	162	1 GLBH_CHITH	P12550 chironomus
35	33	53.2	162	1 GLBH_CHITP	P29242 chironomus
36	33	53.2	349	1 ALF1_CHLPN	Q928Q7 chlamydia p
37	33	53.2	398	1 TRWD_BRUME	O8Y1L6 brucella me
38	33	53.2	430	1 MAS1_AGRP9	P50202 agrobacteri
39	33	53.2	475	1 EXL_ECOLI	P04995 escherichia
40	33	53.2	505	1 SMIL_YEAST	P32566 saccharomyc
41	33	53.2	562	1 EXG2_YEAST	P52911 saccharomyc
42	33	53.2	610	1 CC20_YEAST	P26309 saccharomyc
43	33	53.2	713	1 CDG2_PAENA	P31835 paenibacill
44	33	53.2	921	1 SYL_BACSU	O45477 bacillus su
45	33	53.2	923	1 AGLU_TETPY	O00906 tetrahymena

ALIGNMENTS

RESULT 1

ID	APOH_HUMAN	STANDARD	PRT	345 AA
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)			
DE	(Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).			
GN	APOH OR B2G1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=91315408; PubMed=1650181;			
RA	Steinkasserer A., Estaller C., Weiss E., Sim R.B., Day A.J.;			
RT	*Complete nucleotide and deduced amino acid sequence of human beta 2-			
RT	glycoprotein I.;			
RL	Biochem. J. 277:387-391(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=92008618; PubMed=1655523;			
RA	Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen R.R.,			
RA	Moeller K.B., Moeller N.P.H., Sottrup-Jensen L.;			
RT	*Molecular cloning and mammalian expression of human beta			
RT	2-glycoprotein I cDNA.;			
RL	FEBS Lett. 289:183-186(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=92084151; PubMed=1748314;			
RA	Mehdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,			
RA	Peeples M.E.;			
RT	*Nucleotide sequence and expression of the human gene encoding			
RT	apolipoprotein H (beta 2-glycoprotein I).;			
RL	Gene 108:293-298(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=92273779; PubMed=1339416;			
RA	Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N.,			
RA	Werner P., Arnaud P.;			
RT	*Molecular cloning and sequence analysis of the cDNA encoding human			
RT	apolipoprotein H (beta 2-glycoprotein I).;			
RL	Int. J. Clin. Lab. Res. 21:256-263(1992).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=92135065; PubMed=1777418;			
RA	Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,			
RA	Iasura T., Koike T.;			
RT	*Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by			
RT	cDNA cloning and inter-species differences of beta 2-GPI in			
RT	alternation of antidiolipin binding.;			

Int. Immunol. 3:1217-1221(1991).

16]

RA SEQUENCE FROM N.A.

RA MEDLINE-99115472; PubMed-9914524;

RA Okkels H., Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;

RT "Structure of the human beta2-glycoprotein I (apolipoprotein H)

RT gene.";

RT Eur. J. Biochem. 259:435-440(1999).

RT [7]

RA SEQUENCE FROM N.A.

RA TISSUE=Liver;

RA MEDLINE-22388257; PubMed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RT [8]

RA SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

RA MEDLINE-84222015; PubMed-6587378;

RA Lozier J., Takahashi N., Putnam F.W.;

RA "Complete amino acid sequence of human plasma beta 2-glycoprotein I.";

RA Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).

RA [9]

RA SEQUENCE OF 20-38.

RA TISSUE=Follicular fluid;

RA MEDLINE-21148139; PubMed-11250549;

RA Aleporou-Marinou V., Pappa H., Yalouris P., Patargias T.;

RT "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein

RT from human follicular fluid.";

RT Comp. Biochem. Physiol. 128B:537-542(2001).

RT [10]

RA DISULFIDE BONDS IN C-TERMINAL DOMAIN.

RA MEDLINE-93050249; PubMed-1426288;

RA Steinkasserer A., Barlow P.N., Willis A.C., Kertesz Z.,

RA Campbell I.D., Sim R.B., Norman D.G.;

RA "Activity, disulphide mapping and structural modelling of the fifth

RT domain of human beta 2-glycoprotein I.";

RT FEBS Lett. 313:193-197(1992).

RT [11]

RA STRUCTURE OF CARBOHYDRATES.

RA MEDLINE-97299942; PubMed-9155091;

RA Gambino R., Ruiu G., Pagano G., Cassader M.;

RT "Qualitative analysis of the carbohydrate composition of

RT apolipoprotein H.";

RT J. Protein Chem. 16:205-212(1997).

RT [12]

RA X-RAY CRYSTALLOGRAPHY (2.7 ÅNGSTRÖMS).

RA TISSUE=Plasma;

RA MEDLINE-99437994; PubMed-10508150;

RA Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,

RA Schouten A., Sliemers M.J.A., Derksen R.H.W.M., Kroon J., Gros P.;

RA "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids

RT based on its crystal structure.";

RT EMBO J. 18:5166-5174(1999).

RT [13]

RA X-RAY CRYSTALLOGRAPHY (2.87 ÅNGSTRÖMS).

RA MEDLINE-20031634; PubMed-10562535;

RA

RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,

RA Laggner P., Prasil R.;

RT "Crystal structure of human beta2-glycoprotein I: Implications for

RT phospholipid binding and the antiphospholipid syndrome.";

RL EMBO J. 18:6228-6239(1999).

RL [14]

RA VARIANT LEU-266.

RA MEDLINE-93273313; PubMed-8099061;

RA Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.;

RT "Human beta 2-glycoprotein I: molecular analysis of DNA and amino

RT acid polymorphism.";

RT Hum. Genet. 91:401-402(1993).

RN [15]

RA VARIANT ASN-107.

RA MEDLINE-97369481; PubMed-9225969;

RA Sanghera D.K., Kristensen T., Hamman R.F., Kamboh M.I.;

RT "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)

RT protein polymorphism.";

RL Hum. Genet. 100:57-62(1997).

RN [16]

RA VARIANTS GLY-325 AND SER-335.

RA MEDLINE-97217791; PubMed-9063752;

RA Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;

RT "Identification of structural mutations in the fifth domain of

RT apolipoprotein H (beta 2-glycoprotein I) which affect phospholipid

RT binding.";

RL Hum. Mol. Genet. 6:311-316(1997).

CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES

CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT

CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING

CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

CC -1- SIMILARITY: Contains 4 Sushi (SCR) domains.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: X58100; CAA41113.1; -

CC EMBL: X53595; CAA37664.1; -

CC EMBL: X57847; CAA40977.1; -

CC EMBL: X62839; AAS1766.1; -

CC EMBL: S80305; AAB21330.1; -

CC EMBL: Y11493; CAA72279.1; -

CC EMBL: Y11493; CAA72279.1; JOINED.

CC EMBL: Y11495; CAA72279.1; JOINED.

CC EMBL: X53595; CAA72279.1; JOINED.

CC EMBL: Y11496; CAA72279.1; JOINED.

CC EMBL: Y11497; CAA72279.1; JOINED.

CC EMBL: Y11498; CAA72279.1; JOINED.

CC EMBL: Y17754; CAA76845.1; -

CC EMBL: BC020703; AAH20703.1; -

CC EMBL: BC026283; AAH26283.1; -

CC PIR: S17178; NEHU.

CC PDB: 1QUB; 08-OCT-99.

CC PDB: 1C1Z; 19-NOV-99.

CC PDB: 1G4F; 28-MAR-01.

CC PDB: 1G4G; 28-MAR-01.

CC Genew; HGNC:616; APOH.

CC MIM; 138700;

CC InterPro: IPR000436; Sushi_SCR_CCP.

CC Pfam: PF00084; sushi; 4.

CC SMART: SM00032; CCP; 4.

CC Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal;

CC Polymorphism; 3D-structure.

CC SIGNAL

CC 1 19

CC 20 345

CC 22 80

CC 23 80

CC 24 80

CC 25 80

CC 26 80

CC 27 80

CC 28 80

CC 29 80

CC 30 80

CC 31 80

CC 32 80

CC 33 80

CC 34 80

CC 35 80

CC 36 80

CC 37 80

CC 38 80

CC 39 80

CC 40 80

CC 41 80

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CC 69 80

CC 70 80

CC 71 80

CC 72 80

CC 73 80

CC 74 80

CC 75 80

CC 76 80

CC 77 80

CC 78 80

CC 79 80

CC 80 80

CC 81 80

CC 82 80

CC 83 80

CC 84 80

CC 85 80

CC 86 80

CC 87 80

CC 88 80

CC

Query Match 90.3%; Score 56; DB 1; Length 345;
 Best Local Similarity 90.9%; Pred. No. 0.0011; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KDKATFGTHDG 11
 ||||| |||
 Db 227 KDKATFGCHDG 237

RESULT 2

APOL_MOUSE STANDARD; PRT; 345 AA.
 ID APOL_MOUSE
 AC Q01339;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI).
 DE (Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).
 GN APOL OR B2GPI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92372000; PubMed=1339387;
 RA Nonaka M., Matsuda Y., Shiroishi T., Moriwa K., Natsume-Sakai S.;
 RT "Molecular cloning of mouse beta 2-glycoprotein I and mapping of the
 RT gene to chromosome 11.";
 RL Genomics 13:1082-1087(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/J; TISSUE=Liver;
 RX MEDLINE=9442017; PubMed=751402;
 RA Seilar G.C., Steel D.M., Zafirooulos A., Seery L.T.,
 RA Whitehead A.S.;
 RT "Characterization, expression and evolution of mouse beta 2-
 RT glycoprotein I (apolipoprotein H).";
 RL Biochem. Biophys. Res. Commun. 200:1521-1528(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Kristensen T.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
 CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -1- SIMILARITY: Contains 4 Sushi (SCR) domains.
 CC
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 CC EMBL; D10056; BAA00945.1;
 CC EMBL; S70439; AAB30789.1;
 CC EMBL; Y11356; CAA72190.1;
 CC PIR; A43286; NEMS.
 CC HSP; P02749; 1C1Z.
 CC MGD; MGI:88058; Apoh.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00084; sushi; 4.
 CC SMART; SM00032; CCP; 4.
 KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
 FT DOMAIN 22 80 SUSHI 1.
 FT DOMAIN 83 138 SUSHI 2.
 FT DOMAIN 141 201 SUSHI 3.
 FT DOMAIN 204 261 SUSHI 4.
 FT DOMAIN 263 345 SUSHI-LIKE.
 FT DISULFID 23 66 BY SIMILARITY.
 FT DISULFID 51 79 BY SIMILARITY.
 FT DISULFID 84 124 BY SIMILARITY.
 FT DISULFID 110 137 BY SIMILARITY.
 FT DISULFID 142 188 BY SIMILARITY.
 FT DISULFID 174 200 BY SIMILARITY.
 FT DISULFID 205 248 BY SIMILARITY.
 FT DISULFID 234 260 BY SIMILARITY.
 FT DISULFID 264 315 BY SIMILARITY.
 FT DISULFID 300 325 BY SIMILARITY.
 FT DISULFID 307 345 BY SIMILARITY.
 FT CARBOHYD 162 162 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 252 252 G -> R (IN REF. 2).
 SQ SEQUENCE 345 AA; 38619 MH; C83F8A6EBD51C940 CRC64;
 Query Match 74.2%; Score 46; DB 1; Length 345;
 Best Local Similarity 80.0%; Pred. No. 0.12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KDKATFGTHD 10
 ||||| |
 Db 227 KDKATFGCHG 236
 RESULT 3
 YB35_SCHPO STANDARD; PRT; 1310 AA.
 ID YB35_SCHPO
 AC O14340;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Oxyesterol-binding protein homolog C2F12.05C.
 GN SPBC2F12.05C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Spouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

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RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT *The genome sequence of Schizosaccharomyces pombe.*;
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: BELONGS TO THE OSBP FAMILY.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 3 ANK repeats.
CC -----
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DR EMBL; Z97211; CAB10154.2; -
DR PIR; T40135; T40135.
DR GenDB_Spombe; SPBC2F12.05c; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000648; Oxysterol_BP.
DR InterPro; IPR001849; PH.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF01237; Oxysterol_BP; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00248; ANK; 3.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS01013; OSBP; FALSE_NEG.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Hypothetical protein; Lipid transport; Transport; ANK repeat; Repeat.
FT REPEAT 54 84
FT REPEAT 88 118
FT REPEAT 188 217
FT REPEAT 254 349
FT DOMAIN 1310 AA; 148474 MW; E6F284F09C073262 CRC64;
SQ SEQUENCE 1310 AA; 148474 MW; E6F284F09C073262 CRC64;

Query Match 67.7%; Score 42; DB 1; Length 1310;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKATFGTHD 10
DB 362 DNASEGTHD 370

RESULT 4
APOH_RAT
ID APOH_RAT STANDARD; PRT; 297 AA.
AC P26644;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
DE (Beta(2)GPI).
GN APOH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=8936680; PubMed=2771654;
RA Aoyama Y., Chan Y.L., Wool I.G.;
RT *The primary structure of rat beta 2-glycoprotein I.*;
RL Nucleic Acids Res. 17:6401-6401(1989).
CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

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CC -1- SIMILARITY: Contains 4 Sushi (SCR) domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X15551; CAA33556.1; -
DR PIR; S05310; NBRT.
DR HSSP; P02749; ICI2.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 3.
DR SMART; SM00052; CCP; 3.
KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
FT SIGNAL 1 19
FT CHAIN 20 297
FT DOMAIN 20 32
FT DOMAIN 35 90
FT DOMAIN 93 153
FT DOMAIN 156 213
FT DOMAIN 215 297
FT DISULFID 36 76
FT DISULFID 62 89
FT DISULFID 94 140
FT DISULFID 126 152
FT DISULFID 157 200
FT DISULFID 186 212
FT DISULFID 216 267
FT DISULFID 252 277
FT DISULFID 259 297
FT CARBOHYD 69 69
FT CARBOHYD 114 114
FT CARBOHYD 135 135
FT CARBOHYD 145 145
FT CARBOHYD 205 205
SQ SEQUENCE 297 AA; 33197 MW; 911209DA6C119D59 CRC64;

Query Match 66.1%; Score 41; Length 297;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
DB 179 KDKAVFGCHE 188

RESULT 5
APOH_CANFA
ID APOH_CANFA STANDARD; PRT; 345 AA.
AC P33703;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
DE (Beta(2)GPI).
GN APOH.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RX MEDLINE=93221500; PubMed=7682067;
RA Sellar G.C., Keane J., Mehdi H., Peoples M.E., Browne N.,
RA Whitehead A.S.;
RT *Characterization and acute phase modulation of canine apolipoprotein
H (beta 2-glycoprotein I).*;
RL Biochem. Biophys. Res. Commun. 191:1288-1293(1993).
CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES

```

CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -1- SIMILARITY: Contains 4 Sushi (SCR) domains.
 CC -----
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 CC -----
 CC EMBL; X72933; CAA51438.1; --
 CC PIR; JN0465; JN0465.
 CC HSP; P02749; IC1Z.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00084; sushi; 4.
 CC SMART; SM00032; CCP; 4.
 CC Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
 CC SIGNAL 1 19 BY SIMILARITY.
 CC CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
 CC DOMAIN 22 80 SUSHI 1.
 CC DOMAIN 83 138 SUSHI 2.
 CC DOMAIN 141 201 SUSHI 3.
 CC DOMAIN 204 261 SUSHI 4.
 CC DOMAIN 263 345 SUSHI-LIKE.
 CC DISULFID 23 66 BY SIMILARITY.
 CC DISULFID 51 79 BY SIMILARITY.
 CC DISULFID 84 124 BY SIMILARITY.
 CC DISULFID 110 137 BY SIMILARITY.
 CC DISULFID 142 188 BY SIMILARITY.
 CC DISULFID 174 200 BY SIMILARITY.
 CC DISULFID 205 248 BY SIMILARITY.
 CC DISULFID 234 260 BY SIMILARITY.
 CC DISULFID 264 315 BY SIMILARITY.
 CC DISULFID 300 325 BY SIMILARITY.
 CC DISULFID 307 345 BY SIMILARITY.
 CC CARBOHYD 253 253 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 345 AA; 38403 MW; E0B2624879B74FEA CRC64;
 CC SEQUENCE 345 AA; 66.1%; Score 41; DB 1; Length 345;
 CC Query Match Best Local Similarity 70.08; Pred. No. 1.2;
 CC Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC -----
 CC Qy 1 KDRATGCTHD 10
 CC |||||:|||
 CC Db 227 KDRMYGCHD 236
 CC -----
 CC RESULT 6
 CC APOH_BOVIN STANDARD; PRT; 345 AA.
 CC AC P17690; Q28052;
 CC DT 01-AUG-1990 (Rel. 15, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
 CC DE (Beta(2)GPI).
 CC GN APOH.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RA Gao B., Virmani M., Romm E., Lazar-Wesley E., Sakaguchi K.,
 RA Appella E., Kunos G., Takacs L.;
 RA Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Liver;
 RX MEDLINE-92232647; PubMed-1567819;
 RA Bendixen E., Halkier T., Magnusson S., Sottrup-Jensen L.,
 RA Kristensen T.;
 RT "Complete primary structure of bovine beta 2-glycoprotein I:
 RT localization of the disulfide bridges.";
 RN Biochemistry 31:3611-3617(1992).
 RC TISSUE=Liver;
 RP SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC TISSUE=Plasma;
 RX MEDLINE-92089075; PubMed-1751487;
 RA Kato H., Enjoji K.-I.;
 RT "Amino acid sequence and location of the disulfide bonds in bovine
 RT beta 2 glycoprotein I: the presence of five Sushi domains.";
 RN Biochemistry 30:11687-11694(1991).
 CC SEQUENCE OF 20-41.
 CC MEDLINE-90226328; PubMed-2327984;
 CC Li O., Blacher R., Esch F., Congote L.F.;
 CC "Isolation from fetal bovine serum of an apolipoprotein-H-like
 CC protein which inhibits thymidine incorporation in fetal calf
 CC erythroid cells.";
 CC Biochem. J. 267:261-264(1990).
 CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
 CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -1- SIMILARITY: Contains 4 Sushi (SCR) domains.
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 CC -----
 CC EMBL; L07303; AAA30382.1; --
 CC EMBL; X60065; CAA42669.1; --
 CC PIR; JN0502; NBBO.
 CC HSP; P02749; IC1Z.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00084; sushi; 4.
 CC SMART; SM00032; CCP; 4.
 CC Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
 CC DOMAIN 22 80 SUSHI 1.
 CC DOMAIN 83 138 SUSHI 2.
 CC DOMAIN 141 201 SUSHI 3.
 CC DOMAIN 204 261 SUSHI 4.
 CC DOMAIN 263 345 SUSHI-LIKE.
 CC DISULFID 23 66
 CC DISULFID 51 79
 CC DISULFID 84 124
 CC DISULFID 110 137
 CC DISULFID 142 188
 CC DISULFID 174 200
 CC DISULFID 205 248
 CC DISULFID 234 260
 CC DISULFID 264 315
 CC DISULFID 300 325
 CC DISULFID 307 345
 CC CARBOHYD 92 92
 CC CARBOHYD 162 162
 CC N-LINKED (GLCNAC...)
 CC N-LINKED (GLCNAC...)

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .)
 FT CONFLICT 101 101 E -> G (IN REF. 1)
 FT CONFLICT 108 108 F -> S (IN REF. 1)
 FT CONFLICT 177 177 H -> R (IN REF. 1)
 FT CONFLICT 191 191 H -> N (IN REF. 3)
 FT CONFLICT 194 194 W -> C (IN REF. 1)
 FT CONFLICT 259 259 S -> N (IN REF. 1)
 FT CONFLICT 302 302 H -> N (IN REF. 1)
 FT CONFLICT 305 305 K -> R (IN REF. 1)
 FT CONFLICT 329 329 H -> R (IN REF. 1)
 SQ SEQUENCE 345 AA; 38252 MW; E117DAB609461C33 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 345;
 Best Local Similarity 70.0%; Pred. No. 1.9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
 || || || || |
 Db 227 KDTATFGCHE 236

RESULT 7
 DP3B_SPICI STANDARD; PRT; 363 AA.
 ID DP3B_SPICI
 AC P34029;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase III, beta chain. (EC 2.7.7.7).
 GN DNAN.
 OS Spiroplasma citri.
 OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 OC Spiroplasmataceae; Spiroplasma.
 OX NCBI_TaxID=2133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=88A2HP;
 RX MEDLINE=94290261; PubMed=7764984;
 RA Ye F., Renaudin J., Bove J.M., Laigret F.;
 RT "Cloning and sequencing of the replication origin (oric) of the
 RT Spiroplasma citri chromosome and construction of autonomously
 RT replicating artificial plasmids.";
 RL Curr. Microbiol. 29:23-29(1994).
 CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
 CC THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
 CC IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-
 CC INDEPENDENT) ALONG DUPLEX DNA (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: N' deoxynucleoside triphosphate - N diphosphate
 CC + (DNA)(N).
 CC -1- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
 CC epsilon and theta chains) that associates with a tau subunit. This
 CC core dimerizes to form the POLIII' complex. POLIII' associates
 CC with the gamma complex (composed of gamma, delta, delta', psi and
 CC chi chains) and with the beta chain to form the complete DNA
 CC polymerase III complex (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -----
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 CC -----
 CC EMBL; Z19108; CAA79522.1; -
 CC PIR; S35733; S35733
 CC InterPro; IPR001001; DNA_polIII_beta.
 CC Pfam; PF00712; DNA_pol3_beta; 1.

DR Pfam; PF02767; DNA_pol3_beta.2; 1.
 DR Pfam; PF02768; DNA_pol3_beta.3; 1.
 DR SMART; SM00480; POL3bc; 1.
 DR TIGRFAMS; TIGR00663; dnan; 1.
 KW TRANSFERASE; DNA-directed DNA polymerase; DNA replication.
 SQ SEQUENCE 363 AA; 41329 MW; C969A39BEFEF26D6 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 363;
 Best Local Similarity 72.7%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 11
 || || || || ||
 Db 39 KDKITFTSDG 49

RESULT 8
 F123_CORVE STANDARD; PRT; 283 AA.
 ID F123_CORVE
 AC O74631;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Protein FDD123 (CVHSP30/1).
 GN FDD123.
 OS Corioliolus versicolor.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corioliolus.
 OX NCBI_TaxID=57466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO 30340;
 RX MEDLINE=97398356; PubMed=9256254;
 RA Iimura Y., Tatsumi K.;
 RT "Isolation of mRNAs induced by a hazardous chemical in white-rot
 RT fungus, Corioliolus versicolor, by differential display.";
 RL FEBS Lett. 412:370-374(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ARCHAEAL OPSIN FAMILY. HSP30
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AB003518; BAA33053.1; -
 CC EMBL; AB018406; BAA76590.1; -
 CC HSP; P02945; 1BEX.
 CC InterPro; IPR001425; Bac_rhodopsin.
 DR Pfam; PF01036; Bac_rhodopsin; 1.
 DR PRINTS; PR00251; BACTRLOPSIN.
 KW Transmembrane.
 FT TRANSMEM 24 44 POTENTIAL.
 FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 97 117 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 148 168 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 217 237 POTENTIAL.
 FT DOMAIN 106 113 POLY-LEU.
 FT DOMAIN 194 197 POLY-LEU.
 SQ SEQUENCE 283 AA; 30992 MW; E9E777C00D24818D CRC64;

Query Match 61.3%; Score 38; DB 1; Length 283;
 Best Local Similarity 70.0%; Pred. No. 3.8;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KDKATFGTHD 11
 || || || || ||

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Db      243 DYATFGLHSG 252

RESULT 9
DEXB_STREQ
ID DEXB_STREQ STANDARD; PRT; 537 AA.
AC Q59905;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase)
DE (Exo-1,6-alpha-glucosidase) (Glucodextranase).
GN DEXB
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H46A;
RX MEDLINE=94049672; PubMed=8232196;
RA Medhold U., Steiner K., Vettermann S., Malke H.;
RT "Genetic organization of the streptokinase region of the
RT Streptococcus equisimilis H46A chromosome.";
RL Mol. Gen. Genet. 241:129-140(1993).
CC -1- FUNCTION: The physiological substrates may be short
CC isomaltosaccharides (By similarity).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in 1->6-alpha-D-glucans and derived oligosaccharides.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL; X72832; CAA51348.1; --
CC DR PIR; S39970; S39970.
CC DR HSP; P21332; I00K.
CC DR InterPro; IPR006589; Alp_aml_cat_sub.
CC DR InterPro; IPR006047; Alpha_aml_cat.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR SMART; SM00642; Amy; 1.
CC DR Hydrolase; Glycosidase.
CC SQ SEQUENCE 537 AA; 61733 MW; 154DF0ACAF302FC7 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 537;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKATFGTHD 10
Db 222 NQATFGNHD 230

RESULT 10
Y690_VIBCH
ID Y690_VIBCH STANDARD; PRT; 307 AA.
AC Q9R039;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein VC0690.
GN VC0690.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN-EI Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Giddison R.J., Haft D.H., Hickey E.K., Peterson J.D., Unyam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Niermann R.D., Fleischmann R.D., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -1- SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
CC -----
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CC -----
CC EMBL; AE004155; AAF93855.1; --
CC DR TIGR; VC0690; --
CC DR HAMAP; MF_00068; --; 1.
CC DR InterPro; IPR005486; GCKR.
CC DR InterPro; IPR005488; GCKR_like.
CC DR InterPro; IPR001347; SIS.
CC DR Pfam; PF01380; SIS; 1.
CC DR TIGRPFAM; TIGR00274; TIGR00274; 1.
CC DR PROSITE; PS01272; GCKR; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 307 AA; 32730 MW; CF4F4790BB9C5EA6 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 307;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10
Db 121 EDNATLGAHD 130

RESULT 11
TRMU_YEAST
ID TRMU_YEAST STANDARD; PRT; 417 AA.
AC Q12053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
DE (EC 2.1.1.61).
GN YDL033C OR D2761.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA Paulin L., Saren A.M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA - S-adenosyl-L-
CC homocysteine + tRNA containing 5-methylaminomethyl-2-
CC thiouridylate.
CC -1- SIMILARITY: BELONGS TO THE TRMU FAMILY.
CC -----
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DR EMBL; M14773; AAA49261.1;

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron

DR EMBL; M14773; AAA49261.1;

RA Choi S.K., Codani J.J., Connerthoff A., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Hollsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: Autolysins are involved in some important biological
 CC processes such as cell separation, cell-wall turnover, competence
 CC for genetic transformation, formation of the flagella - in
 CC particular of its basal body - and sporulation. Has a high
 CC affinity for teichoic acid-endowed peptidoglycan.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl
 CC residues and L-amino acid residues in certain bacterial cell-wall
 CC glycopeptides.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
 CC FAMILY 3.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; M87645; AAA22581.1; -;
 CC DR EMBL; M81324; AAA22371.1; -;
 CC DR EMBL; D10388; BAA01225.1; -;
 CC DR EMBL; 299122; CAB15579.1; -;
 CC DR PIR; B41322; B41322; -;
 CC DR Subtilist; BG10407; lytC.
 CC DR InterPro; IPR002508; Amidase_3.
 CC DR Pfam; PF01520; Amidase_3; 1.
 CC DR Pfam; PF04122; CW_binding_2; 3.
 CC DR SMART; SM00646; Ami_3; 1.
 CC KW Competence; Sporulation; Hydrolase; Cell wall; Membrane; Repeat;
 KW Signal; Complete proteome.
 KW SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 496 N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLB.
 FT DOMAIN 30 318 3 X TANDEN REPEATS.
 FT REPEAT 30 128 1.
 FT REPEAT 129 222 2.
 FT REPEAT 223 318 3.
 SQ SEQUENCE 496 AA; 52625 MW; 146FF36B41BB5EC5 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 496;
 Best Local Similarity 63.68; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 KDKATGTHDG 11
 |||||

Db 480 KDKAAQATHDG 490
 RESULT 14
 PHSG_BACSU STANDARD; PRT; 798 AA.
 ID P39123;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycogen phosphorylase (EC 2.4.1.1).
 GN GLGP.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=94195107; PubMed=8145641;
 RA Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
 RT "Glycogen in Bacillus subtilis: molecular characterization of an
 RT operon encoding enzymes involved in glycogen biosynthesis and
 RT degradation.";
 RL Mol. Microbiol. 11:203-218(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98048467; PubMed=9387221;
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 RT in the 200 kb rnb-dnaB region.";
 RL Microbiology 143:3431-3441(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogawara N., Mosser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Chou S.K., Codani J.J., Connerthoff A., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Hollsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
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 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwa A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terptrtra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
 CC CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN
 CC THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.
 CC HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
 CC PROPERTIES.
 CC -1- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate =

CC ((1.4)-alpha-D-glucosyl(N-1) + alpha-D-glucose 1-phosphate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON
CC SOURCES THAT ALLOW EFFICIENT SPORULATION
CC -1- SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
CC -----
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CC -----
CC EMBL; Z35795; CAA01044.1;
CC EMBL; AF008220; AAC00218.1;
CC EMBL; Z91119; CAB15072.1;
CC PIR; S40052; S40052.
CC HSSP; P06738; LYGP.
CC Subtilist; BG10911; glgP.
CC InterPro; IPR000811; Glyco.trans_35.
CC Pfam; PF00343; phosphorylase; 1.
CC PROSITE; PS00102; PHOSPHORYLASE; 1.
CC Transferase; Glycosyltransferase; Allosteric enzyme;
CC Carbohydrate metabolism; Glycogen metabolism; Pyridoxal phosphate;
CC Complete proteome.
CC BINDING 646 646 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 798 AA; 91755 MW; 2E5FD08F05C75045 CRC64;
CC -----
Query Match 58.1%; Score 36; DB 1; Length 798;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 TFGTHDG 11
DB 654 TIGTHDG 660

RESULT 15
UL70_MCMVS
ID UL70_MCMVS STANDARD; PRT; 964 AA.
AC Q69153;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Helicase/primase complex protein (Probable DNA replication protein
DE UL70).
GN UL70.
OS Murine cytomegalovirus (strain Smith).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=10367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96082764; PubMed=7483291;
RA Messerle M., Rapp M., Lucin P., Koszinowski U.H.;
RT "Characterization of a conserved gene block in the murine
RT cytomegalovirus genome."
RL Virus Genes 10:73-80(1995).
CC -1- FUNCTION: INVOLVED IN DNA REPLICATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
CC EBV-1 7, EBV BSF1, HVS-1 56, VZV 6, HCMV AND MCMV UL70.
CC -----
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CC -----
CC EMBL; L07319; AAA96665.1;
CC InterPro; IPR004340; UL52_UL70.

DR Pfam; PF03121; UL52_UL70; 1.
KW Helicase; DNA replication.
SQ SEQUENCE 964 AA; 109704 MW; 70605300E1D85864 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 964;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 ATFGTHDG 11
DB 160 STYGTGHEG 167

Search completed: August 28, 2003, 18:35:07
Job time : 6.66667 secs